Homework 3

1. Please go to the following link to find the SSW library:
   https://github.com/mengyao/Complete-Striped-Smith-Waterman-Library
2. Find the /src/ssw.c for the implementation in C of the Striped Smith
   Waterman algorithm as your reference.
   (https://academic.oup.com/bioinformatics/article/23/2/156/205631)
3. Write a software using a modern C++ SIMD library (e.g., simdpp:
   https://github.com/p12tic/libsimdpp) that can perform pairwise alignment
   with the Striped Smither Waterman algorithm.
   a. INPUT: Two sequences (i.e., Seq1 and Seq2) in the FASTA format
      (https://en.wikipedia.org/wiki/FASTA_format), it is OK to assume no
      newline in a sequence.
   b. OUTPUT: BLAST like output but simplified

```
Speedup: 0.4X
Seq1:      453    CCAATGCCACAAAACATCTGTCTCTAACTGGTG--TGTGTGT    492
                  |||   ||| ||||  |||||| | ||| |||||  |*|||||
Seq2:       17    CCA--GCC-CAAA--ATCTGT-TTTAA-TGGTGGATTTGTGT     51


                  "|": match
                  " ": indel, add gaps "-" in the corresponding sequences.
                  "*" : mismatch
```

The speedup is calculated against the time needed for the regular banded
Smith-Waterman implementeation without SIMD, which means that you need to
implemented both versions (i.e., w/ and w/o SIMD).

```cpp
#include<queue>
#include<functional>
#include<iostream>
Void add()
{
        std::cerr<<"1"<<std::endl;
}

struct ADD
{
        void operator()()
        {
                std::cerr<<"2"<<std::endl;
        }
};

int main(void)
{
        ADD a;
        std::queue< std::function<void(void)> > jobs;
        jobs.push( std::bind(add) );
        jobs.push( std::bind( std::bind(a) ) );
        jobs.push( std::bind(a) );

        while(!jobs.empty() )
        {
            jobs.front()();
            jobs.pop();
        }
        return 0;
}
```